

FIG. 1

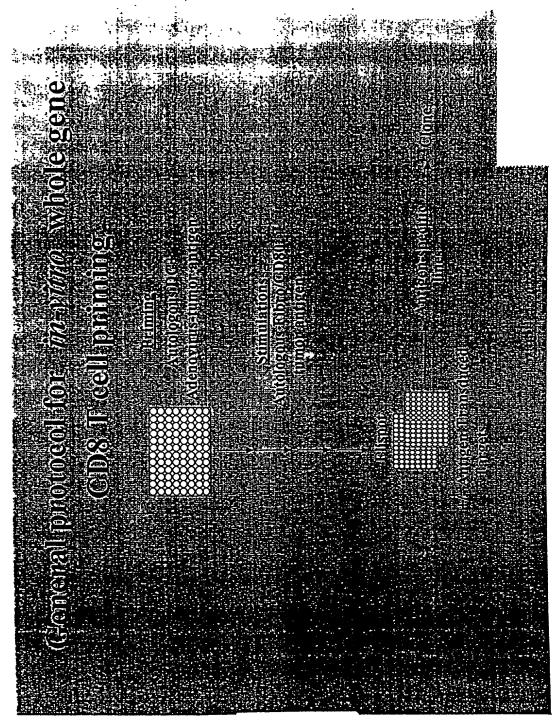


FIG. 2

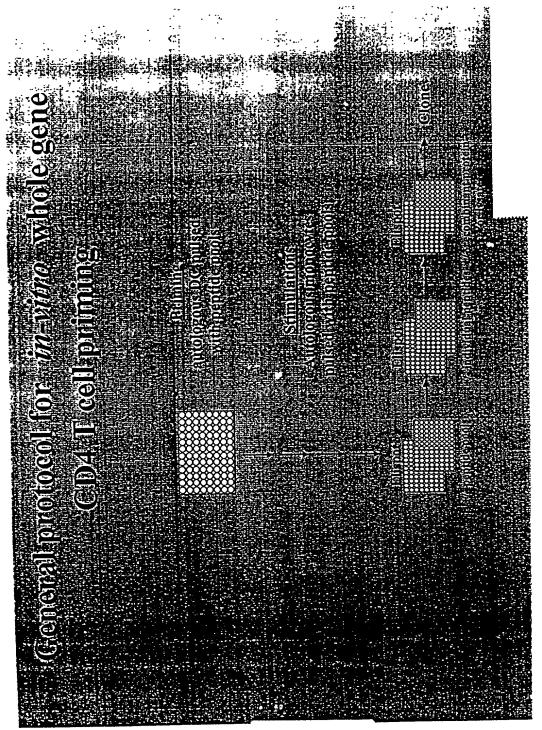


FIG. 3

LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		C	y5 Probe
715540	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell		SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	T	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell		1006	Colon N
Lymphoma, B cell		SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell		S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cel			
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.

RED: Normal essential tissue probes where gene expression is to be avoided.

BLACK: Normal tissue probes where gene expression is acceptable.

High Differenti	High Differential Expression in Group 1 All Lymphomas > N comparison for Lymphomas	Sroup 1 1 for Lymphon	nas	All Mean	All Mean Signal 1 > 0.3 Threshold : 3		Gendank	Second Ninediae)		tuEST	Cetabs	Detabs Tumor Ag	Disclos. <1.e-25	GenSeq <1.9-25 <	Filing <1.e-25
0	90	Patent	ď	Ratio	Mean Signal 1	Mean Signal 2	22		Constant Automotive Constant C	200			:	*******	
No.	No. : 0.1		5	1			,	770000		14 (991537)	7		7		3
201		202	334	20.63	1.596	0.077	∯ .to	13591713	lg superfamily receptor translocat, assoc. protein 2c (IRTA2)	(20) 12000954	KO T	0 0	4 4	•	N M
10,303	0.5 K0432 FT	5 5	32.5	8.97	0.532	0.059	. 60	7705303	hypothetical protein (BM-009)	77 (8266743)	4 å	s c	- 2	i (n	. ~
4.01	10,487 R0408 A10	505/528	588	8.97	0.313	0.035	60	13752361	ADP-ribosylation factor binding protein GGAZs	03 (12663422)	2	0	9	o	
10,534	34 R0459 D1	505	432	6.79	0.64	0.094	52	32485	heat shock protein hispoo	74 (12798470)	-	0	-	4	-
10,500	00 R0424 C3	528	486	6.62	4.	90.0	φ,	10438409	hypothetical protein DKFZp564K0822 (DKFZP564K0822)	111 (12946011)	7	0	7	8	₹ !
10,4	0,495 R0417 D10	505	25	60.0	0.571	0.080	• "	13775193	hypothetical protein DKFZp434B195	38 (7850181)	80	0	= .	0 0	٠.
5.01 5.01		519	3 5	5.63	3 5	0.00	·	5263056	DNA seq. from done RP3-437M21 on Chr. 22q13.2-13.33	0	- (0 0	- ‹	.	- +
10,504		£ \$	017	2 7	0.355	0.078		2576344	Chr. 16 BAC done CIT987SK-A-735G6, complete	15 (1275016)	7	-	v •	۰ د	- ~
10,488	88 R0408 D/ 97 po444 E	\$ 5	506	4	0.30	0.077	· ო	7940357	Chr. 22q11 done b461k10, complete seq.	85 (11592124)	m 4	.	າແ	4 0	4
10,471		8 8	456	3.8	0.305	0.077	က	14550413	ig superfamily receptor translocationassociated 2 (IRTA2)	2 (12000954)	٥٦	,	> 4	. 4	• •
10,499		528	528	3.89	0,328	0.084	11	13652932	protein x 0004 (LOC51184), mRNA	09 (13283830)	• -	, ,	۰ م	· - -	က
10,4		228	<u>8</u>	3.75	0.355	0.085	က	14150032	hypothetical protein DKFZp761B1514 (DKFZp761B1514)	61 (11063636)	- un	• •	ı vo	0	7
10,493	93 R0414 H4	202	637	3.55	0.313	0.088	71	10047288	mRNA for KIAA1607 protein, partial cos	1 (12070889)	2	0	2	٥	~
10,508	08 R0436 A3	505	610	3.21	0.308	9600	٥								
	0				į		Ş	73677	rearranged to kappa light chain variable region(1.26)	250 (13547215)	101	0	7	62	9 :
10,525		25	378	11.05	1.664	101.0	§ \$	20773	B lymphocyte antigen CD20 (B1, Bp35)	10 (6866994)	-	0	-	8	£ 3
10,523		505	616	10.75	1,565	0.140	ž È	33741	rearranged immunoglobulin lambda light chain	2 (12909772)	-	0	-	0 (8 9
10,528		\$ S	279	5.07	99.7	0.170	<u> </u>	29773	B lymphocyte antigen CD20	40 (12019778)	ო	0	m ·	۰ ،	\$:
10,51		8 8	7 9	5.5 5.8	1 117	0.113	± 2	29773	B lymphocyte antigen CD20 (B1, Bp35)	7 (11592147)	es !	0 (m ‡	.	ξ τ
10,020		8 8	737	3 8	1 204	0.124	0	0	0	0 (ლ ,	> 0	÷ •	• •	? ~
515 01	3 R0421 C1	97 97	35	9.47	1.374	0.145	24	703088	MHC class II DPw3-alpha-1 chain	0	- 4	,	- 40	, c	. g
10,524		5 6	5	8.25	1.537	0.186	=	29773	B tymphocyte antigen CD20 (B1, Bp35)	16 (12902627)	۰ ٦	, c	o vo		32
10.522		209	222	7.71	1.29	0.167	165	536774	germline IGLV3S2 gene for ig lambda variableregion	9 (0103024)	r vo		, ro	0	9
10,527		505	576	6.84	1.131	0.165	5	29773	B lymphocyte antigen CD20 (B1, Bp35)	20 (10162753)		. 0	2	-	-
10,533		505	\$	6.19	0.826	0.133	က	7020973	CDNA FLU20705 its, GONE (AIA) 2.5	8 (565914)	,	0	7	-	-
10,530	_	248	475	5.5	0.731	0.133	e	10439253	CDNA: FLJZZ/4/ iis, done rawy izo	0	· 00	0	o,	0	6
10,496	96 R0421 A3	228	595	5.23	0.984	0.188	۰ ،	0	a lumphoode antiden CD20	0	7	0	7	0	15
10,520		505	52	4.45	0.73	0.164	φ (29//3	DNA sed from clone RP11-29716 on Chr. 13, completesed.	38 (11593033)	ო	0	7	2	۰ ۲۵
10,509		505	8 3	\$ 9	0.646	0.16 80.16	N 6	14550413	Ig superfamily receptor translocationassociated 2 (IRTA2)	6 (5886479)	-	0		0 (4 0
10,519		8 8	9 4	2 0	43.0	3 4	, .	o	0	27 (1933024)	4	0	on 2	>	5 ه
10,491		8 3	5 5	8 4	0.72	5 5	2	11433251	KIAA0101 gene product (KIAA0101), mRNA	213 (13456724)	27	1 (05975)	% %	٠ ،	<u> </u>
10,469	04 D046 C0	2 2	¥ \$	3 6	0.472	0.13	~	10438413	cDNA: FLJ22139 fis, done HEP20959	67 (10817681)	7 7	.	9 ¢	۰ د	> 2
10,486		516	524	3.43	0.592	0.173	12	11433251	KIAA0101 gene product (KIAA0101), mRNA	162 (13264392)	Q -	,	: -	• 0	٠
10.5		528	388	3.24	0.428	0.132	-	12858505	M. musculus adult male cecum cDNA, RIKEN full-length enricheditor.	34 (5802642)	- ^		~ ~	0	s
10,5		528/505	8	3.21	0.485	0.151	0	0		51 (0092042)	. 89	0	12	60	7
10,490		505/528	589	3.1	0,366	0.118	*	13752361	ADP-nbosylation factor binding protein 60724	13 (10035232)	-	0	1	-	-
10,511	11 R0437 G11	505	929	3.03	0.439	0.145	m	14249329	Typotrania prominenta					,	ş
	0.2		101	37.3	3 324	0.577	=	29773	B lymphocyte antigen CD20	1 (2898616)	- ;	۰ ،	- 3	o ¥	ē ç
2 5	_	8	ş	2 7	6.308	1.362	555	33741	rearranged immunoglobulin lambda light chain	233 (13442196)	Ξ,	o 6	₫ •	3 <	<u> </u>
10,01		8 8	2 2	4.33	101	0.234	0	0	0	59 (1191101)	, c	-	, c	· -	· -
. · ·	10,501 RO423 AS	3 2	678	4.32	1.394	0.323	-	12001993	clone 014b03 My026 protein mRNA	126 (8168503)		, ,	211	4	128
10.531			251	4.31	1.744	0.405	50	33741	rearranged immunoglobulin lambda light chain	4 (6838748)			-	0	15
10,512			292	4.29	2.147	0.5	9	179307	B-lymphocyte cell-surface antigen B1 (CU20)	(04/9000) (ო	0	¥
10,536	_	528	507	4.24	0.978	0.231	^	4506044	proteogrycan 1, secretary grannie (*1701)	13 (12770918)	ო	0	6	0	33
10,510		\$	510	4.2	7.328	1.74	= 4	29773	O lymphocyte arwae i conduct d	51 (7044121)	ω	0	7	0	4
10,5		505	420		0.81	0.222	> 8 —	14777681	immunoglobulin lambda joining 3 (IGLJ3)	100 (14068988)	103	0	102	56	123
10,514		228	8		6.874	5.5	ß c		0	0	ო	0	က	0	ກ
10;	0,502 R0425 A5	228	433	3.33	3	3	>	,	1						

					1.			Genbank Describited					
	9	0	Q C	Mean Signal 1	Mean Signal 2								
Seq.	Element (96)		Naud	1000					04 (0704280)		0	က	
ID No.	JU.7	380	40.12	0.307	9000	0		hu repeat	K7 (13285739)		0	-	8
	200	27.4	37.21	0.406	0.011	-	5262709	mRNA; cDNA DKFZp586N1323	19 (6603577)		0	7	0
70,01	AU (1400	Ş	18.27	0.394	0.022	12	13642967	poly(A)-binding protein, cytoplasmic 1 (PABPC1)	37 (40399002)	-	0	-	-
4/0,01	20442 80	2 2	12.58	0.368	0.027	0	0	0	St (10000000)	-	0	-	0
10,033	200100	3 8	12.1	0.455	0.038	7	9506672	hypothetical protein (FLJ20323), mkNA	46 (41503033)	· 10	0	က	•
	NOT 10 100	3 8	0.67	0.554	0.057	~	12584450	DNA seq. from clone RP11-297/6 on Chr. 13	24 (7008550)		0	80	~
	K0432 A11	29/	9.0	0.873	660.0	176	5926696	Genomic, chromosome 6p21.3, HLA Class I region	(140363060)	· -	. 0	-	•
10,01	K0441 B1	700	9 9	0.244	0.051	0	0	0	(ecesozo) +	٠,		ო	e
	R0412 C9	3	000	- C	2000		11493464	clone FLC0675 PRO2870 mRNA	159 (12604620)			. +	•
	R0408 E10	519	5,33	0.332	7000	. •	12000431	12 BAC RP11-61286	1 (7113300)	-	> 0	- ‹	
10,562	R0438 B1	38 4	4.55	0.324	0.071	-	12000431	protessome (prosome, macropain) subunit, beta type	14 (10399152)	7	0 1	7	۰ ،
	R0439 D6	471	4.4	0.36	0.082	2 ,	12653014	mRNA for KIAA0625 protein, partial cds	29 (1280909)	-	٥	7	1
10,551	R0410 G11	530	3.44	0.328	0.095	,	3327003					•	•
ľ	0.1 - 0.2							14 Total action of the second	4 (12674085)	က	0	8	-
	POLET AS	231	10.19	1.761	0.173	22	219402	eukaryonc initianori jacos 75.	1 (13290909)	-	0	-	0
10,576	82 96700	165	7.76	5,1	0.193	33	13279085	RAN, member RAS oncogene ramily	4 (8304077)	4	0	4	•
10,567	01 00101	}		1.053	41.0	÷	5566605	MIF2 suppressor (HSMT3)	(40606443)	• 64	0	4	-
10,565	R0438 C4	350		3 5	45.	25	184231	non-histone chromosomal protein HMG-14 gene	(01407071) 06	, ;	• •	ď	-
10,580	R0459 F1	653	0.87	3 5	2 4	٠ -	c	0	22 (11155912)	≥ .	- 6	. +	c
10,545	R0410 A7	375	6.5	6.60	2 5		12803596	hypothetical protein FLJ20647, clone MGC:3443	10 (13129911)	- :	> <	. ç	
10,540	R0408 D1	233	4.97	0.612	0.123	- ;	4506236	protessome activator subunit 2 (PA28 beta) (PSME2)	148 (14067253)	*	5 '	2 .	, •
10.560	R0428 D9	522	4.17	0.768	0.184	S ·	0070004	House the transfer of the Property of the Prop	0	4	•	n i	- (
10.577	R0457 B7	453	3.97	0.47	0.118	·	1354057	-CNA EL 122478 file clone HS114935	38 (12428993)	က	0	7	,
10,556	R0416 A7	33	3.91	0.423	0.108	6	10440178	COLOR Chr 22011 2 clone KB1269D1	4 (2968224)	-	0	-	> '
10.550	R0410 F10	298	3.9	0.435	0.112	es	5103007	genomic Divo, Oill Etg. 1000	96 (12708451)	က	0	ო	m
10,543	R0409 B7	305	3.87	0.509	0.131	-	4500154	TRIAN, COLOR TRANSPORTOR COLOR	38 (12945863)	5	0	5	0
10,557	R0416 D12	546	3.85	0.416	0.108	φ	10437682	CDIAC, PLUZ 1904 iis, cicii Colored Co	125 (12800010)	o,	0	~	· ·
10.544	R0409 D12	583	3.71	0.569	0.153	+	14329055	Chromosome o Glorid C. Common	93 (12787237)	6	0	80	ر
10,570	R0459 D2	342		0.513	0.14	-	6807703	CDNA UNITAGE STATE (1.1.1.)	•	7	0	7	0
10,563	R0438 C1	377		0.419	0.117	~	2598184	regulator of G protein signalian grows	35 (2910384)	4	0	-	-
10,549	R0410 E1	358		0.347	0.1	•	0	000000000000000000000000000000000000000	117 (12333933)	9	0	9	7
10,559	B0417 F7	455		0.35	0.102	es	10438346	CDNA: PLJ22084 fis, cione ner 14520	19 (8159998)	∞	0	4	0
10,554	P0413 A5	364	3.4	0.346	0.102	•	0	> (22 (8362796)	8	0	က	0
10,538	D0407 R1	369	3.29	0.414	0.126	•	0	(1270) (1	59 (11681430)	-	0		-
10,539	D0407 D4	188		0.321	0.101	~	6102860	mRNA; cona DKFZp434P171 (done DN72p434F171)	1 (12155967)	-	0	-	_
10,566	20428 54	2 2		0.416	0.132	•	13633789	hepatocellular carcinoma-assoc. antigen bo (nchoo)	32 (1137727)	-	0	-	0
10,537	ROADS HS	662		0.321	0.107	3	2661068	clone 23785 mKNA seq.	, , , , , , , , , , , , , , , , , , , ,				
1	20					_	•		7 (2006441)	-	0	-	7
09301	D0439 C11	678	13.02	3.704	0.285	5	14124943	nbosomai protein th	38 (10731492)	10	0	νo	0
00001	D0440 B8	408		4.045	0.38	-	10185402	DNA seq. from clone RP11-432Mz4 on Citi. 13	239 (14055451)	∞	0	S	S
10,240	00438 040	467		1.95	0.25	45	14141173	high-mobility group (nonhistone chrom.) protein 2(nmc2)	44 (42727100)	• ••	0	o	-
10,01	DOMAN F11	= =		2.361	0.369	135	13436316	tubulin alpha 6)	101	0	00	0
10,578		430		3.701	0.69	0	0	0	3 (5436308)	80	0	80	0
0,5,01		2 6		0.905	0.221	4	5566605	MiF2 suppressor (HSMT3)	34 (8657449)	. 2	0	က	7
10,547		3 8		0.757	0.205	2	7022980	CDNA FLJ10754 fis, clone N12RP3004544	65 (12387261)	=	0	7	0
10.558	R0417 C5	499		1.776		-	5817076	cDNA DKFZp58601224 (from clone UNT Cpusos) (12-1)	115 (12765428)	=	0	o	9
10,575	R0445 D10			1,965		7	13638568	Successe sensitive element billoning protein (1907)	45 (3400628)	၉	٥	6	٥
10,571	B0440 H9		3.21	0.816	0.254	٥	0	O					
			ł					Figure 6					

Figure 6

Hematology therapeutic Ab candidates

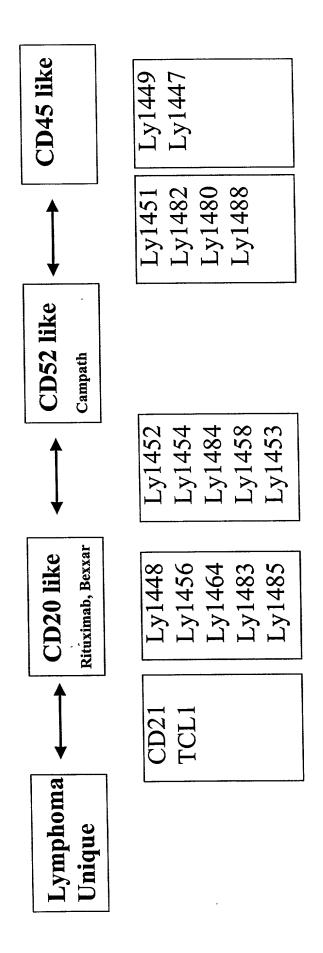


Figure 7

Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

.L* AML	-/+			١	++	-/+ ++++		ı. n.d.	<u>'</u>	J. n.d.	J. n.d.	d. n.d.	d. n.d.	d. n.d.	d. n.d.	d. n.d.	+++++++++++++++++++++++++++++++++++++++			+++	•
eloma CL	‡	+		+		‡	+++++	n.d.	n.d.	n.d.	n.d.	l. n.d.	n.d.	l. n.d.	. n.d.	i. n.d.	++++	+++	n.d.	‡	+
Hodgkin Myeloma CLL*	+	+++		<u>. </u>	++	+	+	+ n.d.	++	+ n.d.	+ n.d.	- n.d.	+ n.d.	+ n.d.	++ n.d.	++ n.d.	+++ +++	+	++ n.d.	+	++
Ly	+++			+++	+++		++, T-NHL		+++	+++	+++	++	+++	+++	+++	+++	+++, T-NHL	+	++	++	-
CD2+	1		•	1	•	8	+	•	+	+	+		+	+	‡	+++	‡		+		77
CD14+			1	8		1							‡	‡	<u>+</u>	‡	‡		+		77
CD19+	+++++++++++++++++++++++++++++++++++++++		+	+	* + +	‡ ‡ ‡	‡	+++	+++	‡	‡	++++	++	‡	+	‡	++	+	+++	‡.	777
CD34+				1				ı				-	+	+	+	++	++	‡	‡	++	
Gene	0000	ביבי	CDZ1	TCL1	LV1448	LM452	Lv1456	Ly1464	Ly1483	Lv1458	Ly1481P	Ly1485P	Ly1480	Ly1488	1 1 484	1 1482	Ly1453	Lv1449	Lv1447	Lv1451	22.0

. Ω†π SEQ IDNO.

Ly1447 sequence:

CCTTCAACAĞACTGGATGGGGTCCACCCACATTAGGGTGGAGTTTGTTCTGCCACTGTGCAGTTATCATTCTGGGATGGG GGTACCTTACTCTCCCAATGAGAAATTCTAAATTTCCTCTTTTGAGCCTGGTGCCTCCACCTTCTCANAACTGCATAGGG CTGTCCTTCTTGACTTCAACTAGGCCTAAAAAAGCGN

Ly1448 Sequence

10,562

 $\hbox{$\tt CCAGGGTTAGGACATTCAAATGTCTTTATCCACATTCCTGAAGGATAATTGTTATAGATTCCCTACCTCCATAGGAATGC}\\$ TTATAATGGATTATCTATACAATCTCCACATTCCCACATTTTGCATTAGAGAATGGAATCAGTCAAACCCTGTTCCCAGA GTTTCCCTTAGAGTTCTCACCTGTTGTCTTATATCCATCTAGGAATCCCCATCTCTAATGTAAGCTTGGAGATCCGGGCC CCCGGGGGACAGGTGACTGAAGGACAAAAACTGATCCTGCTCTGCTCAGTGGCTGGGGGTACAGGAAATGTCACATTCTC TGAAAGAGAGTGATGCCGGCAAATATTACTGTAGAGCTGACAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATATC CCTGTGAGAAGACCTGATGGCTATAGAAGAGACCTCATGACAG

SEDIDNO:

Ly1449 Sequence

10,583

CCACATTGGGAATTCTGCACACAGGTGCCTGCTCCACCANNCAGAGAGGCTCAGGAGATTGTCCAGGGACAAGGAGACCT GGCCGGACCTCTGCAGGGAGGTGAGGCCCCTGCCCCCATCTTGTCCCATCACATTCTGGATGTTTGGCATCCCCAGGCTC AGCCTCACAGCCTCTTTCTCAGATGCAGTCACCACTTTACCAAACTTGGCACATCCAACCACTCCTTTCATAATTTTACA ${\tt CCTGTTTGTGGCCTGGCTGACAGATATTTTGTNATTGATCTTTCTAATTTCAGGGATTCTAAATGTGTTTTGAGAATCTG}$ GTCAGCACTCANGGATTCTGTCTTT

SED ID NO:

10,584

SECTIONO:

10,585

SERTONO

10,586

SEQIONO.

10,587

Ly1451 Sequence CTGCTGCTAAATACCTNTGAGAAACTCTGCTTCTATCTAAGGGGACCTACTTTTNTCNGGAATCTCAATACTTGGAACAA GAACCTCCTANACGGACCCTTTGGCATAATGAATTGGACCAACTGTAGGTTCCAGGACTAGAGAGCCAGCAATGCCTCCA TGAACAATCTCACCCAATTACTCTGCTCAGGAAACGAGGTAACTGATGGACAGCCGAGGCAGCCCCTTAGGCGGCTTAGG

Ly1452 Sequence

AÄAANACCAÄTAGCAGCCAAAACAGAACATTTGTAAACAAAACCACAACTATCAGCCCTGTGCTTAAACACAGAATCTGC ATTCTTTTGAAACATTAAGTATATGCAATAAAGAGAATATAGACCATCTTTTTCCTTAATATACAATACCCAATATCTAA AACAATGTCACCAATAATAGACACAAATCGGTGTTATCATAAGGCATGTTGAACAGTCTTTTTCACAGTACTCAGGGGGCA TCATGGGGCTGCAGAGGCCACACTTTCCAGAAGTTTTCTCCTCGCTGTGATCCTCGCACACCGGGGGCACTCGGAGGACT GGAAGCACTGTTTGTGAAAGCAAGCCCTGCACGCTGAACATCTTCTACATGTTGCTGTCTGAAATGGGAAGATGACAGTC AATGTCCTTGAGTAAGGGTGCCAGCAGCCCTTTCTTGATCCTGACCAGGTCCTCAAGGGAGAACAGGTGGAGCTCATCAG TCAAGTGTCCCGGCCTGCCCTACAAACTCCTTTAATGCACTGTTAGCAAACCTACAGGTCTTCAACAGCTTCTTGATAT

GGAAGAGCTGCTCCTGAATTTCCTTC

Ly1453 Sequence

CCAAAAACTTCAGCATAAAAACTATCCTGTCTGTGTATTATATATTTTATTACTNNATTTAATAAACAAAAACCACTTT TGAACCAGGTAATTTTATCTAGTGTGAAAAGAAATTAATCACATGGTCATATACTGGCTAGTGCTCTCTAAAAGTAGACA ${\tt TTAAAATATTTCATAATTGGAGGGAATCTTTGGAGATTAGTGGCATCTAATCTTGGGGCCTCAGACACCCCAAAATCTATA}$ TATTGACCAGTGGAAGTTGATGATTTGTTATCAAATTTCAAAGCACCTAATGGAAACCCCACTTCATCTCTGTGAAGATT TTCAGTNCCTTTACAGTTATTTGAAATTATTTCAATTCTGTGGAGCCACTTCAGAAACTCCAATGGGCCTTTGCAATATT AAAATGTGGAGAATGCATTAATCATTATTTAATCAATGAGTTT

CAGAAGCTACCAAATCTTTATGTTTGAAGTCATGCACCATCTTTTCCACGAGTATCCTGTTGATTATTTTGATCAGCTTG TTCAGTCTGGGAGGGAATTGCACAAGGGCATGAATACTCCACTGGCAAGGATCATTGGGGGCCATCTTGGAAGCTGTGTG AATGAGCAAATGAATGCACAGATAGAATATTAGCAGTGACAATGATGCTAGAGGTCACCTACCCCACTGTCCTCTTGTCC TTCTCCCCCAACCCTCCCCTGCTCCCAGGCAAGAAGCCCTCTAGCCTCTGCTTGATCACTTTCAGCACTCAACATCTTCA GGGAACCTATTCCGCCGTGGGACAGTGTTAATTAGTGGAAAACTCTTTTTCAAAAGTTGAAATCAGTTCCTCTGTGTCTA

TTACCTGCTGATCACTGTCCAGACTTCTGGAGGACACAGAGCAAGTTTTATTCCTCTTACTGATGGTAGCCTTTCAGATC CATCCCTTCCCTCCAGTATATTAGAGTTACGTAAATTCTTAAAATGCTTAGCAGCTCATTTATCCTGAACA

SER TO NO: 10.588

Ly1456 Sequence

añagacatgâaaaatatcccaagatcatactagatcataatagcaattcctttacaaatgaattatggaggtaactgatc TCTAACAGTTTCCTTCATGTTGTTTTAATGCACAAGGGCAGAGGATCTGCCGACCCTTGGAACCAGCGTGAGCTAACCAC TAGTAGCCCACCCCCGCTGCTCCAAAACTTGAGTTGTTTCAAATGTTTCTCACTGTTCATCTCTNCACTGACCCCACTC CAGAAAGCCTGGAGAGAGGCCAAGATGCCACCCACCTTCCCCAATCCCTCGCCACAGATCTGTGTCTATCACACACTCTG TAAGTGCCGCTTTGCTTCTTCCTCTTGAAAAGACTGAGAACACACATTTTAACATGTTANGAAAATGGGGCAGGCTAA

AAAATGACTGATCCCACCGCCAGTGACTCA

SEQIDNO:

10, 585

Ly1458 Sequence TTGAATGCTCTATTTTGCNNTAANNNTTTATTNACTAGTCTCAGTAATACATTAGTAAAAANCATGTCNCTTAATTAATT GGGTTANAATCAAANAAACATANAGTNGGGCAATATACTTNATCCTACCCATCCCACCCAAATCTTACTCTACTCATNTC ATTCTCATTAATTTTGGGAAANCATNANAANATGGGTTCGTTGAGTAANANATTAAAANAAATAAGCTTTTTGATCCCTGCCAACACCCCCATGCCCAGGGGGGGCACCCCTCCAATACAATAACATGCCAGGAANAGTAAGNTGCCCTTTCTGANGCCGNA ATCTGCCATCATNTTCCCATNTTCCAGNCTNTTTCCATTGCNAGNCACAATCTGGGTCTCAGGGATNATACCCGGTCTTA

> Figure 9 Page 1 of 2

SED IDNO: 10,590

Ly1464 Sequence

aaagagaactaatggaagtggattgaatacagcagtctcaactgggggcaattttgcccc ccagaggacattgggcaatgtttggagacattttggtcattatacttggggggttggggg

atggtgggatgtgtg

SECTONO 10,591

Ly1480 Sequence $\hbox{\tt CTGTAGCCTCTGCAAGTGAAAATCCAGGCCGACTTGCAGTCATTGGACTGATGTCCAAGTGCAATCACCATACAGCAGCT}$

AACACACTGTTTTCTGTGATAGAAACTGTCGGCCCTGCTGGGGGACAAGATATTCACGGCCTCACTAGCCAGTGAGATGC CACCAGGGCGGCCTGCCCCTGATGCTCCTTTGTTACCTGCTAAAGAAGGACCATAAGGTAAAAGGCACCTTACCTTATGGAGTGAGCCCAGGCCAGGGAAAAGCTTGGGTAGAACAATCCAAGGGGCAGCCTGGGTGTGAGAATCCAGCCCAAGCTAG

CTGCTCTAGAAGCCTGGAGG

ZEOZDND: 10,542

Ly1482 Sequence

GCTTATTCCTCTGCACGGACTCGGAGACGGTCCTCAGCGGGAGGAGCTCAGGTCTCCCTGGGCCAGACACGTGCCCCAGA

SECTIONS.

10,593

Ly1483 Sequence

GCTGGAGCTTCACTGTGAGTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTTATCACGAGGATGACACCTTGGGGA ${\tt TTACCRCTGCGGGAATCACGGGGCTGGTGSTCARCATCYTCGTCCTTGYWGCTGCTGCTGCTGCTGCATTACGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCA$

SER IANO

10 डेंब्स

Ly1484 Sequence

GGGGTTTCTTCTGTAGGCAGAGCTCAGGCCCCAGTCACCTCTGCCACCCTCAGCCTGGCACTGTTGTGCCAGAGCCTCTG $\tt CTTGTGTCCCATGGGGCCCTCCATCAGGCAGCAACAGGTTATGGCTCCTTCTGGGCCCCAGGCTGTGGTGATGCTGG$

SED ID NO:

1055

Mi

CTGTCTCCACTGTGGAGTTACTATTTTTCCTTTTCCCCATTTTATTCATCAGAAGCCAGTCACTAAGCGAGGTCAAACTC TGTTTCTCCTCTAAAAAACTCTTTAATCCTTTTAAGCCTCAATTTCTTAATTGTGAAATGGGGCTAATACCTGTATCCAA CCAAGGGAGTAGTTAGAAGGTAACATGATAGGTGGAAAGCACTTAACATAGGCAAAATGTTATTATCAGGAATGATCGAG AGACCCATCCAACTATCTGAAGGAGTCACTTAACTCTACTGTACTGCAAGCGCTGTAAAGTCLTGCATCTTTCACTGGGG $\tt GTAAAGGCCCCCAGTCCCTGAGACGGGCCAGTTTGGAaGACAGGCTGGTTTTTTCTCTGTTCTCCTGAGAGCCCTTCAGA$ TGAGAAGGGAGGTCTGGAGACAGAATGCCAAAAGCCCATTAAAGGCACGCCTTGCATTTCAGAGAGGGGAGCAGGTCTAG

AGAAGAACCAGAGGAGCTCAG

SERITO NO: 10,596

Ly1488

 $\overline{ ext{CT}}GGYCTGTGGGTGATCCCAGCTCTTACTAGGAGAGGGAASTGAaGGTCYTGGTGCCAGGGGCCCAGGCCCTCCAACCAT$ AAACAGTCCAGGATGGAACCTGGTTCACCCTTCATACCAGCTCCAAGCCCCAKACCATGGGAGCTGTCTGGGATGTTGAT

ACCTGCCCCCAGGTGG

Figure 9 Page 2 of 2

Figure 1a. Ly1464 full length DNA sequence (SEQ IDNO: 10,597)

```
1 gatgcaagga gatgagacag ttaaatttac ttcctctttt ctaatctgag aggtttcatg
  61 ttgaagaaaa tcagtgttgg ggttgcagga gacctaaaca cagtcaccat gaagctgggc
121 tgtgtcctca tggcctgggc cctctacctt tcccttggtg tgctctgggt ggcccagatg
181 ctactggctg ccagttitga gacgctgcag tgtgagggac ctgtctgcac tgaggagagc
241 agctgccaca cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc
301 tacaetttea gigaaeceit ecaeetgatt gigteetaig aeiggeigat eeiceaaggi
361 ccagccaagc cagtttttga aggggacctg ctggttctgc gctgccaggc ctggcaagac
421 tggccactga ctcaggtgac cttctaccga gatggctcag ctctgggtcc ccccgggcct
481 aacagggaat tetecateae egtggtacaa aaggcagaca gegggcaeta eeactgcagt
541 ggcatcttcc agagecetgg teetgggate ecagaaacag catetgttgt ggctateaca
601 gtccaagaac tgtttccagc gccaattctc agagctgtac cctcagctga accccaagca
661 ggaagcccca tgaccctgag ttgtcagaca aagttgcccc tgcagaggtc agctgcccgc
 721 ctcctcttct ccttctacaa ggatggaagg atagtgcaaa gcagggggct ctcctcagaa
781 ttccagatcc ccacagettc agaagatcac tccgggtcat actggtgtga ggcagccact
841 gaggacaacc aagtttggaa acagagccc cagctagaga tcagagtgca gggtgcttcc
901 agetetgetg caceteeeac attgaateca geteeteaga aateagetge tecaggaact
 961 getectgagg aggeceetgg geetetgeet eegeegeeaa eeceatette tgaggateea
1021 ggcttttett eteetetggg gatgecagat ceteatetgt ateaceagat gggeettett
1081 eteaaacaca tgcaggatgt gagagteete eteggteace tgeteatgga gttgagggaa
1141 ttatctggcc accggaagec tgggaccaca aaggctactg ctgaatagaa gtaaacagtt
1201 catccatgat ctcacttaac caccccaata aatctgatte tttattttet ettectgice
1261 tgcacatatg cataagtact tttacaagtt gtcccagtgt tttgttagaa taatgtagtt
1321 aggtgagtgt aaataaattt atataaagtg agaattagag tttagctata attgtgtatt
1381 ctctcttaac acaacagaat tctgctgtct agatcaggaa tttctatctg ttatatcgac
1441 cagaatgttg tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg
1501 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt ggtcattata
1561 cttggggggt tgggggatgg tgggatgtgt gtgctactgg catccagtaa atagaagcca
1621 ggggtgccgc taaacatcct ataatgcaca gggcagtacc ccacaacgaa aaataatctg
1681 gcccaaaatg tcagttgtac tgagtttgag aaaccccagc ctaatgaaac cctaggtgtt
1741 gggctctgga atgggacttt gtcccttcta attattatct ctttccagcc tcattcagct
1801 attettactg acataccagt ctttagetgg tgetatggte tgttetttag ttetagtttg
1861 tatcccctca aaagccatta tgttgaaatc ctaatcccca aggtgatggc attaagaagt
1921 gggcctttgg gaagtgatta gatcaggagt gcagagccct catgattagg attagtgccc
1981 ttatttaaaa aggccccaga gagctaactc acccttccac catatgagga cgtggcaaga
2041 agatgacatg tatgagaacc aaaaaacagc tgtcgccaaa caccgactct gtcgttgcct
2101 tqatcttqaa cttccaqcct ccaqaactat gagaaataaa attctgttgt ttgt
```

Figure 1b.Ly1464 protein sequence (SEQ ID ND: \$10,598)

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPV FEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVP SAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSSA APPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKA TAE

TMpred Report for Ly1464

Date:

SERTONO: 10,598

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTED DLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQ AWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSP GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQR SAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVW KQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPS SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRK PGTTKATAE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains

Transmembrane Domain 1: 3 - 24 Score: 1.5484
Transmembrane Domain 2: 71 - 92 Score: 1.3009
Transmembrane Domain 3: 158 - 179 Score: 1.3027

Ly 1464 MHC class binding peptides (SERID NDs: 10,599-10,819)

Ly1464 Al binding peptides

TATAGA MI DIHO	ing peptides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3		67	67.5
	FSEPFHLIV	52	25
4	LTDAREAGF		
5	SSEDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFQIPTA	222	2.7
8	MPDPHLYHQ	312	2.5
9	LMELRELSG	339	2.25
10	HTEDDLTDA	47	2.25
11	CTEESSCHT	40	2.25
12	ALGPPGPNR	118	2
13	LGMPDPHLY	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	ī
16	LRELSGHRK	342	0.9
17	OLEIRVOGA	255	0.9
		239	0.9
18	WCEAATEDN		0.9
19	SAEPQAGSP	179	
20	AREAGFOVK	55	0.9
Ly1464 HLA A2	binding peptides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLWV	13	4047
2	LLLKHMQDV	323	1006
3	VLMAWALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILQGPAKPV	81	118.2
7	LLGHLLMEL	334	83.53
		25	33.81
8	LLAASFETL		
9	WQDWPLTQV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153 ′	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916
Ly1464 A3 bin	ding pentides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLILQGPAK	79	30
2	ELFPAPILR	167	18
3	ALGPPGPNR	118	9
4	VLWVAQMLL	18	6
5	VLMAWALYL	6	5.4
6	LLKHMQDVR	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSCQTK	187	2
9	LLGHLLMEL	334	1.8
10	GMPDPHLYH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35
		- - -	

Figure 12 Page 1 of 4

14	ALYLSLGVL	11	1.35
15	YLSLGVLWV	13	1.2
16	ATEDNOVWK	243	1
17	HMODVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KAYTFSEPF	63	0.9
20	KOSPOLEIR	251	0.81
20	NOSTQUEIN	231	0.01
Ly1464 Al1	binding peptides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	1
2	WLILOGPAK	79	0.6
3	KOSPOLEIR	251	0.36
4	COTKLPLOR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPQK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLKHMODVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKPGTTK	347	0.06
13	RVQGASSSA	259	0.06
14	LPLORSAAR	196	0.06
15	EFSITVVQK	127	0.06
16	YTFSEPFHL	65	0.06
17	ITVOELFPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKDGR	206	0.04
Ly1464 A24	binding peptides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLLL	317	200
2	VFEGDLLVL	89	30
3	TFYRDGSAL	111	20
. 4	GFOVKAYTF	59	15
5	KPVFEGDLL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVLW	12	9
9	IFQSPGPGI	146	7.5
10	APEEAPGPL	285	7.2
11	TFSEPFHLI	6 6	7.2
12	HLLMELREL	337	6. 6
13	MTLSCQTKL	188	6.6
14	VLMAWALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
. 17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8 4.8
20	DVRVLLGHL binding peptides	330	4.0
PA1404 W00	binding peptides		
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSGHR	. 341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8 8
9	VVAITVQEL WVAOMILAA	160 20	8
10	WVAQMLLAA	20	8

Figure 12 Page 2 of 4

11 12 13 14 15 16 17 18 19 20	GVLWVAQML KQSPQLEIR PTLNPAPQK AVPSAEPQA ETASVVAIT VVQKADSGH WLILQGPAK LLKHMQDVR CQTKLPLQR RVQGASSSA	17 251 270 176 156 132 79 324 192 259	8 7.5 6 6 6 6 5 5 4
RANKIŃG	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20	DVRVLLGHL KPVFEGDLL APEEAPGPL LQRSAARLL QVWKQSPQL VVAITVQEL IVSYDWLIL GVLWVAQML VLMAWALYL MAWALYLSL ALYLSLGVL HMQDVRVLL APGTAPEEA SPMTLSCQT DAREAGFQV RVLLGHLLM HLLMELREL LLGHLLMEL VLWVAQMLL HLYHQMGLL	330 87 285 198 248 160 74 17 6 8 11 327 281 186 54 332 337 334 18	200 80 72 40 20 20 20 21 12 12 12 6 6 6 6 5 4 4
Ly1464 B8 bind			
RANKING 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 Ly1464 B27 bin	SEQUENCE DVRVLLGHL DAREAGFQV LQRSAARLL FSFYKDGRI GCVLMAWAL MAWALYLSL LLGHLLMEL HLYHQMGLL VLMAWALYL AARLLFSFY APILRAVPS ALYLSLGVL HLIVSYDWL LLAASFETL VLWVAQMLL HMQDVRVLL APEEAPGPL LSGHRKPGT GVLWVAQML SSSAAPPTL ding peptides	330 54 198 207 4 8 334 316 6 202 171 11 72 25 18 327 285 345 17 264	THEORETICAL SCORE 8 7.2 1.2 1 0.8 0.8 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4 0.4
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1 2 3 4 5	LRELSGHRK VRVLLGHLL ARLLFSFYK AREAGFQVK QRSAARLLF	342 331 203 55 199	2000 2000 2000 2000 1000

Figure 12 Page 3 of 4

6	GRIVOSRGL	213	600
7	NREFSITVV	125	600
8	KOSPOLEIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	COAWODWPL	99	200
12	LRCOAWODW	97	200
13	HLYHQMGLL	316	150
14	ALYLSLGVL	11	150
15	VLWVAQMLL	18	150
16	COTKLPLOR	192	100
17	VQKADSGHY	133	100
18	LQGPAKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Ly1464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHLIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNREF	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APEEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCOTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
, 20	DAREAGFQV	54	3.6

Ly1464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTOVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKA	56	18
5	EAGFQVKAY	57	13.5
6	LGMPDPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELFPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDAREA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHLIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPVCTEE	35	1.8

Figure 12 Page 4 of 4

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file> LY1464~1.TXT
Beginning with residue: 1 and ending with residue: 359
AMPHI Window size: 11
A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.
5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREA GFQVKAYTFSEPFHLIV
AAAAAA
RRRRRRRRRRRR
DDDDDD
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
SYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQ KADSGHYHCSGIFQSP
АААААААААААААААА
RRRRR
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
${\tt GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYK}$
DGRIVQSRGLSSEF
AAAAAAAAAAAAAAA
RRRRRRRRRRRRRRRRRR
DDDDDDDDDDDDDDDDDD

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPG
TAPEEAPGPLPPPPTPS
AAAAA
RRRRRRRRRR
DDDDDDDDD
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKATA
E
AAA
RRRRRRRRRRRRRRRRRRRR
DDDDDD

Figure 13 Page 2 of 2

Table 4. Immunogenic portions of Ly1464 (SEQIDNDs: 10,820-10,842)

MKLGCVLMAWALYLSLGVLWVAQMLLAASF

LGVLWVAQMLLAASFETLQCEGPVCTEESS

ETLQCEGPVCTEESSCHTEDDLTDAREAGF

CHTEDDLTDAREAGFQVKAYTFSEPFHLIV

QVKAYTFSEPFHLIVSYDWLILQGPAKPVF

SYDWLILQGPAKPVFEGDLLVLRCQAWQDW

EGDLLVLRCQAWQDWPLTQVTFYRDGSALG

PLTQVTFYRDGSALGPPGPNREFSITVVQK

PPGPNREFSITVVQKADSGHYHCSGIFQSP

ADSGHYHCSGIFQSPGPGIPETASVVAITV

GPGIPETASVVAITVQELFPAPILRAVPSA

QELFPAPILRAVPSAEPQAGSPMTLSCQTK

EPQAGSPMTLSCQTKLPLQRSAARLLFSFY

LPLQRSAARLLFSFYKDGRIVQSRGLSSEF

KDGRIVQSRGLSSEFQIPTASEDHSGSYWC

QIPTASEDHSGSYWCEAATEDNQVWKQSPQ

EAATEDNQVWKQSPQLEIRVQGASSSAAPP

LEIRVQGASSSAAPPTLNPAPQKSAAPGTA

TLNPAPQKSAAPGTAPEEAPGPLPPPPTPS

PEEAPGPLPPPPTPSSEDPGFSSPLGMPDP

SEDPGFSSPLGMPDPHLYHQMGLLLKHMQD

HLYHQMGLLLKHMQDVRVLLGHLLMELREL

VRVLLGHLLMELRELSGHRKPGTTKATAE

Researcher:

LY1464 and recombinant Ra12-LY1464

Alex Gaiger, Aijun Wang, Jonathan Clapper

Reference: cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was Description:

cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, Ra12-LY1464, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction

screening.

Protein Diagram of Ra12-LY1464

N-term 6x His tag -

- Nco I linker - 1994 1994 64

Cloning Strategy:

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Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and Ly1464antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separted on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 Ra12-LY1464. This ligation mixture was used to transform competent E. coli Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant Ra12-LY1464 in E. coli.

Cloning Primers:

LY1464-sense

5' - CGTCCATGGACatgaagetgggetgtgteete - 3' (SEQID NO:10,843)

21bp 57%GC 56C Tm prime full length 32bp 59%GC 68C Tm

LY1464-antisense

5' - CCTTCTCGAGctattcagcagtagcctttgtggtc - 3' (SEQIDNO:10, 844)

25bp 48%GC 58C Tm prime full length 35bp 51%GC 67C Tm

Protein Expression:

Various E. coli strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For Ra12-LY1464, The most optimal expression condition is pCRX2 Ra12-LY1464 in Tuner (DE3) CodonPlus-RP grown in 2xYS media at 37°C induced with 1.0mM IPTG at 25°C (room temp) for 3hr.

DNA/Protein Sequence:

LY1464 (DNA) 1080bp (SEQ IDNO 10,845)

atgaagctgggctgtgtcctcatggcctgggccctctacctttcccttggtgtgctctgggtggcccagat gctactggctgccagttttgagacgctgcagtgtgagggacctgtctgcactgaggagagcagctgccaca cggaggatgacttgactgatgcaagggaagctggcttccaggtcaaggcctacactttcagtgaacccttc cacctgattgtgtcctatgactggctgatcctccaaggtccagccaagccagtttttgaaggggacctgct ggttctgcgctgccaggcctggcaagactggccactgáctcaggtgaccttctaccgagatggctcagctc tgggtcccccgggcctaacagggaattctccatcaccgtggtacaaaaggcagacagcgggcactaccac tgcagtggcatcttccagagccctggtcctgggatcccagaaacagcatctgttgtggctatcacagtcca agaactgtttccagcgccaattctcagagctgtaccctcagctgaaccccaagcaggaagccccatgaccc tgagttgtcagacaaagttgcccctgcagaggtcagctgcccgcctcctcttctccatctacaaggatgga aggatagtgcaaagcaggggctctcctcagaattccagatccccacagcttcagaagatcactccgggtc atactggtgtgaggcagccactgaggacaaccaagtttggaaacagagcccccagctagagatcagagtgc agggtgcttccagctctgctgcacctcccacattgaatccagctcctcagaaatcagctgctccaggaact gctcctgaggaggcccctgggcctctgcctccgccgccaaccccatcttctgaggatccaggcttttcttc tcctctggggatgccagatcctcatctgtatcaccagatgggccttcttctcaaacacatgcaggatgtga gagtcctcctcggtcacctgctcatggagttgagggaattatctggccaccggaagcctgggaccacaaag gctactgctgaatag

Ra12-LY1464 (DNA) 1500bp (SEQ ID NO: 10,467)

atgcatcaccatcaccatcacacggccgcgtccgataacttccagctgtcccagggtgggcagggattcgc cattccgatcgggcaggcgatcgcgggccagatcaagcttcccaccgttcatatcgggcctaccg ccttcctcggcttgggtgttgtcgacaacaacggcaacggcgcacgagtccaacgcgtggtcgggagcgct de constant de la con eaccgcgatggcggacgcttaacgggcatcatcccggtgacgtcatctcggtgacctggcaaaccaagt egggcggcacgcgtacagggaacgtgacattggccgagggacccccggccgaattctccatggacatgaag ctgggctgtgtcctcatggcctgggccctctacctttcccttggtgtgctctgggtggcccagatgctact ggctgccagttttgagacgctgcactgtctgcactgaggagagcagctgccacacggagg atgacttgactgatgcaagggaagctggcttccaggtcaaggcctacactttcagtgaacccttccacctg attgtgtcctatgactggctgatcctccaaggtccagccaagccagtttttgaaggggacctgctggttct gcgctgccaggcctggcaagactggccactgactcaggtgaccttctaccgagatggctcagctctgggtc recccgggcctaacagggaattctccatcaccgtggtacaaaaggcagacagcgggcactaccactgcagt ggcatcttccagagccctggtcctgggatcccagaaacagcatctgttgtggctatcacagtccaagaact gtttccagcgccaattctcagagctgtaccctcagctgaaccccaagcaggaagccccatgaccctgagtt gtcagacaaagttgccctgcagaggtcagctgcccgcctcttctctacaaggatggaaggata gtgcaaagcagggggctctcctcagaattccagatccccacagcttcagaagatcactccgggtcatactg ptgtgaggcagccactgaggacaaccaagtttggaaacagagcccccagctagagatcagagtgcagggtg pettecagetetgetgeaceteceacattgaatecagetecteagaaateagetgetecaggaaetgeteet gaggaggcccctgggcctctgcctccgccgccaaccccatcttctgaggatccaggcttttcttctcctct ggggatgccagatcctatctgtatcaccagatgggccttcttctcaaacacatgcaggatgtgagagtcc teceteggteacetgeteatggagttgagggaattatetggeeaceggaageetgggaecacaaaggetact gctgaatag

Ra12-LY1464 (protein) (SER ID NO: 10,468)

MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSA PAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAEGPPAEFSMDMK LGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHL IVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCS GIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRI VQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAP EEAPGPLPPPPTPSSEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKAT AE.

Protein Info:

Ra12.LY1464

Molecular Weight 53010.15 Daltons 499 Amino Acids 29 Strongly Basic(+) Amino Acids (K,R) 46 Strongly Acidic(-) Amino Acids (D,E) 174 Hydrophobic Amino Acids (A,I,L,F,W,V) 128 Polar Amino Acids (N,C,Q,S,T,Y) 5.663 Isolectric Point -14.119 Charge at PH 7.0

M84 Ly1448. DNA Sequence (SERID NO: 10, 846)

1 agogagaett ceagtocgag gtoctgottt ctgotatga actattocac atgacaagtg 121 otgoccottc tottgocaac atotoctgot toacocaagtga agactgotgal 121 ttgotattga gactgoctot tottaaagga acactgocd 122 tattocacaca agacttotta tgotattoca 123 taataaagt cattottaa tgotattoca 123 taataaagt cattottaa tgotattaa 123 taataaagt cattottaa tgotattaa 123 tattocacaca agagtttoga ttgotagocca agocatgaat gtotacttat catcaagtc 123 ttocacacaa agagtttoga ttgotagocca agocatgaat gtotacttat catcaagtc 123 ttocacacaa agagttoga ttgaaagaa gtoaagaagaaga 124 ttoacacacaa catcaagaag gtyaaagaaa aaagaagaa 125 taagaagttga agagtgoc ttaagatga tottottgg agagactggg 121 tgaagattga agagttcaca cogototggg agagaagaag tgotaaagaagaag 123 tgaagattga agagttcaag cogototggg agagaagaag tgotaaagaagaag 124 taagacactga gagagaagaag tocttoctcag ceatgaagat gstocaagaagaag 125 taagaagaaga taagaagaaga taagaagaagaagaagaagaagaagaagaagaagaagaag							
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3121 gcactgtggt gtgtgtgg gagctcagca tgaccaaagg ccgcccgagg ggcttgcgcc 3181 tccggcaggc cttgtatgga cacacacagg ctgtcacgtg cctggcagcg tcagtcacct 3241 tcagctctct ggtgagcgc tcccaggact gcacctgtat cctgtgggat ctggaccacc 3301 tcaccaccgt gacccgcctg cccgccatc gggaaggaca ctcagccatc accatcagtg 3361 acgtctcagg caccattgtc tcctgtgggg gggagcacatt gtcctgtgg aatgtcaatg 3421 gacagccct ggccagcatc accacagcct gggacacact gtccctgtgg aatgtcaatg 3421 gcatggtag gggcccagca tgggacacaa gccagatcat catcaccggg agtcaagacg 3541 gcatggtccg ggtttggaag actgaggatg tgaagatgtc tgttcctgga cggccagcag 3601 gagaggagcc cctggctcag cctccaagcc caagaggcca caagtgggag aagaacctgg 3661 ccttgagtcg agagctgac gttagcattg ctttgacagg gaagccagca 3721 ccgcagtgac tgctctggcc gtgtccagaa accacacaa actcctggtt ggtgatgaga 3781 ggaggagaat attctgctgg tctgcagaa ggtgactgg ggctgaggac ggaggctct tgccaacag 3901 agaaacccc agggcctct tccccacagt tctcaagga gggcctctgg caatcacagc 3961 tctgcagcc aaccctctcc atggccgatg ggacttctat gaaaaggatg agcacacaa							
3181 teeggeagge ettgtatgga cacacacagg etgteaegtg cetggeageg teagteaect 3241 teageeteet ggtgagegge teecaggaet geaectgtat eetgtgggat etggaeeaec 3301 teacecaegt gaceegeetg eeegeeate gggaaggeat etcageate aceateagtg 3361 aegteteagg gaceattg teetgtgegg gageaeaett gteectgtgg aatgteaatg 3421 gacageecet ggeeageate aceacageet ggggeeaga aggageeata acetgttget 3481 geetgatgga gggeecagea tgggaeaeaa geeagateat cateaecggg agteaagaeg 3541 geatggteeg ggtttggaag actgaggatg tgaagatget tgtteetgga eggeeageag 3601 gagaggagee eetggeteag eeteeaagee caagaggeea eaagtgggag aagaaecetgg 3661 eettgagteg agagetggae gttageattg etttgaeagg gaageeeage aaaaecagee 3721 eegeagtgae tgetetggee gtgteeagaa aceacaeaa acteetggtt ggtgatgaga 3781 gggggagaat attetgetgg tetgeagatg ggtgaetggg geagagaega gagaggeage 3841 geacaacagt geeaggetga gggtgeaga ggtgaetggg geetgagete tgeetaaega 3961 tetgeageee aaceetetee atggeegatg ggaettetat gaaaaggatg agcacacaea							
3241 teagecteet ggtgagegge teccaggaet geacetgtat cetgtgggat etgaceace 3301 teacecaegt gaceegeetg eeegeeate gggaaggeat etcageate accateagtg 3361 aegteteagg caccattgte teetgtgegg gageacaett gteectgtgg aatgteaatg 3421 gacageceet gggeeageate accaageet ggggeeaga aggageeata acctgttget 3481 geetgatgga gggeeagea tgggacaeaa ggeagateat cateaceggg agteaagaeg 3541 geatggteeg ggtttggaag actgaggatg tgaagatgte tgtteetgga eggeeageag 3601 gagaggage cetggeteag ectecaagee caagaggeea caagtgggag aagaacetgg 3661 cettgagteg agagetggae gttageattg etttgaeagg gaageecage aaaaceagee 3721 cegeagtgae tgetetggee gtgteeagaa accaeceaa acteetggtt ggtgatgaga 3781 gggggagaat attetgetgg tetgeagatg ggtgaetgg ggeggaaga gagaggeage agaggetetg 3841 geacaacagt geeaggetga gggtggeaga ggtgaetggg geetgagete tgeetaeaga 3901 agaaaacecee agggeeteet teeceacagt teteaaggaa gggeetetgg caateacage 3961 tetgeagece aaceetetee atggeegatg ggaettetat gaaaaggatg agcacaeca							
3301 teacecacyt gacecycety cecyceate gygaagycat eteagecate accateagty 3361 acytetcagy caccattyte teetytycegy gagcacactt yteetyty aatyteaaty 3421 gacagcect gygeccagcat accacaget gygycecaga aggagcata acctyttyct 3481 geetyatyca gygeccagca tygyacacaa gecagateat catcacegyg ayteagacy 3541 geatycegy gyttygaag actgagyaty tyaagatyte tytteetyga egyccagcag 3601 gagagyagec eetygetcag eetecaagee caagagyeea caagtygyag aagaacetyg 3661 eettyagteg agagetygae gytageaty etttyaacagy gaageecage aaaaccagee 3721 eegeaytyae tyeteetygee gyteecagaa accacacaa acteetygtt gytyatyaga 3781 gygyaagaaat attetyetyg tetycagaty gytagyaaga gagagyeage agagyettety 3841 geacaacagt gecaggetya gygyagaaa gytyaetygg geetyagete tyeetacaga 3901 agaaacecee agggeeteet teecaacagt teteaaggaa gygeeteetyg caatcacage 3961 tetycageec aacceteec atggeegaty gyaettetat gaaaaggaty agcacacaca							
3361 acgtetcagg caccattgte tectgtgegg gagcacaett gtectgtgg aatgteaatg 3421 gacageect ggecageate aceacageet ggggeceaga aggageeata acetgttget 3481 geetgatgga gggeceaga tgggacaeaa gecagateat catcaceggg agteaagaeg 3541 geatggteeg ggtttggaag actgaggatg tgaagatgte tgtteetgga eggecageag 3601 gagaggagee cetggetcag ectecaagee caagaggeea caagtgggag aagaacetgg 3661 cettgagteg aggetggae gttageattg etttgacagg gaageeage aaaaeeagee 3721 eegeagtgae tgetetggee gtgteeagaa aceacaeaa acteetggtt ggtgatgaga 3781 gggggagaat attetgetgg tetgcagatg ggtaggaagg gaaggeage agaggetetg 3841 geacaacagt gecaggetga gggtggeaga ggtgactgg gectgagete tgeetaeaga 3901 agaaaceece agggeeteet tececacagt teteaaggaa gggeetetgg caatcacage 3961 tetgcageec aaceetetee atggeegatg ggaettetat gaaaaggatg agcacaea							
3421 gacagccct ggccagcatc accacagcct ggggcccaga aggagccata acctgttgct 3481 gcctgatgga gggcccagca tgggacacaa gccagatcat catcaccggg agtcaagacg 3541 gcatggtccg ggtttggaag actgaggatg tgaagatgtc tgttcctgga cggccagcag 3601 gagaggagcc cctggctcag cctccaagcc caagaggcca caagtgggag aagaacctgg 3661 ccttgagtcg agagctggac gttagcattg ctttgacagg gaagcccagc aaaaccagcc 3721 ccgcagtgac tgctctggc gtgtccagaa accacaccaa actcctggtt ggtgatgaga 3781 gggggagaat attctgctgg tctgcagatg ggtaggaagg gaaggcagc agaggctctg 3841 gcacaacagt gccaggctga gggtggcaga ggtgactgg gcctgagctc tgctacaga 3901 agaaacccc agggcctcct tcccaacagt tctcaaggaa gggctcttgg caatcacagc 3961 tctgcagccc aaccctctcc atggccgatg ggacttctat gaaaaggatg agcacacaca							
3481 geetgatgga gggeecagea tgggacacaa geeagateat cateaceggg agteaagaeg 3541 geatggteeg ggtttggaag aetgaggatg tgaagatgte tgtteetgga eggeeageag 3601 gagaggagee eetggeteag eetecaagee caagaggeea caagtgggag aagaacetgg 3661 cettgagteg agagetggae gttageattg etttgacaegg gaageecage aaaaceagee 3721 cegeagtgae tgetetggee gtgteeagaa accaecaa acteetggtt ggtgatgaga 3781 gggggagaat attetgetgg tetgeagatg ggtaggaaga gagaggeage agaggetetg 3841 geacaacagt geeaggetga gggtgeaga ggtgactggg geetgagete tgeetacaga 3901 agaaacecee agggeeteet teeceacagt teteaaggaa gggeetetgg caateacage 3961 tetgeageee aaceetetee atggeegatg ggaettetat gaaaaggatg agcaecaca	336.	acgueteage	caccattgto	ceeegegege	gaycacactt	gcccccgcgg	aacyccaacy
3541 gcatggteeg ggtttggaag actgaggatg tgaagatgte tgtteetgga eggeeageag 3601 gagaggagee eetggeteag eeteeaagee eaagaggeea eaagtgggag aagaacetgg 3661 cettgagteg agagetggae gttageattg etttgaeagg gaageeeage aaaaeeagee 3721 eegeagtgae tgetetggee gtgteeagaa aceaeaceaa acteetggtt ggtgatgaga 3781 gggggagaat attetgetgg tetgeagatg ggtageagg agaggeage agaggeetg 3841 geacaacagt geeaggetga gggtgeaga ggtgaetggg geetgagete tgeetaeaga 3901 agaaaceee agggeeteet teeeaacagt teteaaggaa gggeetetgg eaateacage 3961 tetgeageee aaceetetee atggeegatg ggaettetat gaaaaggatg ageacaeaca							
3601 gagaggagce cetggeteag cetecaagee caagaggeea caagtgggag aagaacetgg 3661 cettgagteg agagetggae gttageattg etttgaeagg gaageecage aaaaceagee 3721 cegeagtgae tgetetggee gtgteeagaa aceaeacaa acteetggtt ggtgatgaga 3781 ggggagaaa attetgetgg tetgeagatg ggtagaaga gagaggeage agaggetetg 3841 geacaacagt geeaggetga gggtggeaga ggtgaetggg geetgagete tgeetacaga 3901 agaaacecee agggeeteet teceeacagt teteaaggaa gggeetetgg caateacage 3961 tetgeageee aaccetetee atggeegatg ggaettetat gaaaaggatg agcacacaca							
3661 cettgagteg agagetggae gttagcattg etttgaeagg gaageeeage aaaaceagee 3721 cegeagtgae tgetetggee gtgtecagaa aceacacea acteetggtt ggtgatgaga 3781 gggggaagaat attetgetgg tetgeagatg ggtaggaaga gagaggeage agaggetetg 3841 geacaacagt gecaggetga gggtggeaga ggtgaetggg geetgagete tgeetacaga 3901 agaaacecee agggeeteet tececacagt tetcaaggaa gggcetetgg caateacage 3961 tetgeageec aaceetetee atggeegatg ggaettetat gaaaaggatg agcacacaca							
3721 ccgcagtgac tgctctggcc gtgtccagaa accacacaa actcctggtt ggtgatgaga 3781 gggggagaat attctgctgg tctgcagatg ggtaggaaga gagaggcagc agaggctctg 3841 gcacaacagt gccaggctga gggtggcaga ggtgactggg gcctgagctc tgcctacaga 3901 agaaaccccc agggcctcct tccccacagt tctcaaggaa gggcctctgg caatcacagc 3961 tctgcagccc aaccctctcc atggccgatg ggacttctat gaaaaggatg agcacacaca	360	L gagaggagco	cctggctcag	cctccaagc	c caagaggcca	caagtgggag	aagaacctgg
3721 ccgcagtgac tgctctggcc gtgtccagaa accacacaa actcctggtt ggtgatgaga 3781 gggggagaat attctgctgg tctgcagatg ggtaggaaga gagaggcagc agaggctctg 3841 gcacaacagt gccaggctga gggtggcaga ggtgactggg gcctgagctc tgcctacaga 3901 agaaaccccc agggcctcct tccccacagt tctcaaggaa gggcctctgg caatcacagc 3961 tctgcagccc aaccctctcc atggccgatg ggacttctat gaaaaggatg agcacacaca							
3781 gggggagaat attetgetgg tetgeagatg ggtaggaaga gagaggeage agaggetetg 3841 geacaacagt gecaggetga gggtggeaga ggtgaetggg geetgagete tgeetacaga 3901 agaaaccece agggeeteet tecceacagt teteaaggaa gggeetetgg caatcacage 3961 tetgeageec aaccetetee atggeegatg ggaettetat gaaaaggatg ageacacaca							
3841 gcacaacagt gccaggctga gggtggcaga ggtgactggg gcctgagctc tgcctacaga 3901 agaaaccccc agggcctcct tccccacagt tctcaaggaa gggcctctgg caatcacagc 3961 tctgcagccc aaccctctcc atggccgatg ggacttctat gaaaaggatg agcacacaca							
3901 agaaaccccc agggeeteet teeceacagt teteaaggaa gggeetetgg caatcacage 3961 tetgeageec aaccetetee atggeegatg ggaettetat gaaaaggatg agcacacaca							
3961 tetgeageee aaccetetee atggeegatg ggaettetat gaaaaggatg ageacacaca							
4021 ctcggagggc tgagcagcac gctggaaact gtgacttggt gatgcccagc tgcacacgaa							
	402	r creggaggg	cgagcagca	getggaaae	. grgacrrggt	. gatgcccago	: cgcacacgaa

Figure 17 Page 1 of 2

Ly1484. Protein sequence (long) (SEQ JOND: 10,847)

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF TOKLVEKLYSGMFSADPRHILLFILEHIMVVIETASSQRDTVLSTLYSSL NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ **EOLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR** HKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLLFGHQ HFYICENFTLSPTGDVYCTRHCLSNISDPFIFNLCSKDRSTDHYSCQCHS YADMRELRQARFLLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCSFQP SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTC NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFD VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ DGTVLGDVQLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFGYKQ QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF TKPHPARTAAGKPLPGKDVSTPVSLPGHPQPFFYSLQSLRPSQVTVKDMY LFSLGSESPKGAIGHIVSTEKTILAVERNKVLLPPLWNRTFSWGFDDFSC CLGSYGSDKVLMTFENLAAWGRCLCAVCPSPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHTQAVTCLAASVTFSLLVSGSQDCTCILWDLDHL THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG **EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRN** HTKLLVGDERGRIFCWSADG

Ly1484.Protein sequence (short) (SER ID NO: 10,848)

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVRMPPFTQAFCALQGGSFDVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFIS
LHRKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPFFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRC
LCAVCPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAVTC
LAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG

Figure 17 Page 2 of 2

a. TMpred Report for Ly1484 Long

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF TQKLVEKLYSGMFSADPRHILLFILEHIMVVIETASSQRDTVLSTLYSSL NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK **DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ** eqlfgelglwsqgeetkpcspweldwregparmrkrikrlsplealssgr HKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLLFGHQ HFYICENFTLSPTGDVYCTRHCLSNISDPFIFNLCSKDRSTDHYSCQCHS YADMRELRQARFLLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCSFOP SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTC NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFD VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ ${\tt DGTVLGDVQLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFGYKQ}$ QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF TKPHPARTAAGKPLPGKDVSTPVSLPGHPQPFFYSLQSLRPSQVTVKDMY LFSLGSESPKGAIGHIVSTEKTILAVERNKVLLPPLWNRTFSWGFDDFSC CLGSYGSDKVLMTFENLAAWGRCLCAVCPSPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHTQAVTCLAASVTFSLLVSGSQDCTCILWDLDHL THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG **EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRN** HTKLLVGDERGRIFCWSADG (SEQIDNO: 10841)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVRMPPFTQAFCALQGGSFDVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFIS
LHRKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPFFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRC
LCAVCPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAVTC
LAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG

(SEB ID NO: 10/848)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1484 has 646 amino acids and 1 Transmembrane Domains Transmembrane Domain 1: 102 - 123 Score: 1.3521

> Figure 18 Page 2 of 2

Table2a: Ly1484 long MHC class I binding peptides
(SEQID NO5:10,849-10,908)

HLA A2:		(SEATO NOS: 1	رها الما المام
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
		145	836.3
1	FLLCLMHCL	145 783	818.9
2 3	YLPEFLTNC KLYSGMFSA	57	742.3
4	FILEHIMVV	73	629.3
5	TLYSSLNKV	95	511.9
6	FLQEHWDVV	127	448
7	ILWDLDHLT	1093	431.1
8	ALQGGSFDV	743	403.4 400.9
9	MQYPVFPWV	654 1063	222.6
10 11	ALYGHTQAV YLVRMPPFT	730	188.5
12	CLMHCLLLL	148	181.8
13	GLLSILGFL	120	130
14	VLMTFENLA	1010	118.7
15	ILAVERNKV	973	118.2
16	YLASEKKSL	260	98.27 97.11
17	ELTPEFFYL	776 6 38	84: 56
18	YLMYLNTAA ILLFILEHI	70	73.96
19 20	LLQDIALEI	563	72.72
	nogorman		
HLA A3			
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KLMPGRQAK	292	135
2	VLLPPLWNR	981	60.75 60
. 3	CLGSYGSDK KVILYCLSK	1001 102	54
. 4 5	CVWELSMTK	102	30
6	LLFGHQHFY	495	30
7	PLWEETMLK	247	30
8	FLSPNEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFYNN DR	580	18 13.5
11	KLYSGMFSA	57 3057	13.3
12	GLRLRQALY NLANPKIFR	1057 672	12
13 14	RVWKTEDVK	1183	10
15	QVPKQLFTK	894	9
16	RMPPFTQAF	733	و
17	KLKFIQRFK	694	9
18	RIMLQKWQK	622	9
19 20	VILQELLDK VILQELLDK	. 465 623	9 9 9 6
÷.			
HLA A24			
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	655	300
2	FYICENFTL	502	300 300
3	TYNSNISFL	138	264
4	NYRRRGQEL DYTSETLNL	315 6 65	200
5 6	SYLVRMPPF	729	150
7	RYPGSDRIM	616	75
8	RFLLQDIAL	561	60
9	LYSSLNKVI	96	60
10	YYTHYSSAI	717	50
11	FFPALHESL	443	36 28
12	NFGQVPKQL	891 1004	25
13	SYGSDKVLM GFDDFSCCL	994	24
14 15	EFFYLPEFL	780	24
16	YFYGDRMDL	865	20
17	SFCSFQPSL	594	20
18	RGLRLRQAL	1056	17.28
19	RGQELYASL	319	17.28
20	KNLALSREL	1217	15.84

CID1096 Table 2b.Ly1484 short MHC class I binding peptides (SEQ ID NOS: 10,909 - 10,968)

10010 10111	I SED TO NO	:10 ana -10 916
	(364 1010	
SEQUENCE	STARTING POSITION	THEORETICAL SCORE
YLPEFLTNC ILWDLDHLT ALQGGSFDV MQYPVFPWV ALYGHTQAV YLVRMPPFT VLMTFENLA ILAVERNKV ELTPEFFYL YLMYLNTAA VLADYTSET RMFHSVKST SNFEYLMYL KVLMTFENL LLPPLWNRT QLFTKPHPA GAHLSLMNV WDLDHLTHV	160 470 120 31 440 107 387 350 153 15 39 131 11 386 359 275 507 472	818.9 431.1 403.4 400.9 222.6 188.5 118.7 118.2 97.11 84.56 51.94 45.8 26.76 22.54 21.54 18.38 16.66 15.5
FISLHRKAL CILWDLDHL	469	12.25
SEQUENCE	STARTING POSITION	THEORETICAL SCORE
VLLPPLWNR CLGSYGSDK CVWELSMTK GLRLRQALY NLANPKIFR RVWKTEDVK QVPKQLFTK RMPPFTQAF KLKFIQRFK TILGFVSNF SLPGHPQPF WIDLIFGYK NLHHWIDLI YMQYPVFPW ELTPEFFYL ALYGHTQAV YLPEFLTNC IIVASYLVR DMTVQCHYY QLFTKPHPA	358 378 421 434 49 560 271 110 71 261 301 218 214 30 153 440 160 102 87 275	60.75 60 30 12 12 10 9 9 4.05 3 2.7 2.7 2.7 2.7 2.43 1.5 1.35 1.2
SEQUENCE	STARTING POSITION	THEORETICAL SCORE
QYPVFPWVL DYTSETLINL SYLVRMPPF YYTHYSSAI NFGQVPKQL SYGSDKVIM GFDDFSCCL EFFYLPEFL YFYGDRMDL RGLRLRQAL KNLALSREL KVIMTFENL TFSWGFDDF FYLPEFLIN ANPKIFRDL SFDVADRMF KTSPAVTAL KGRPRGLRL RNKVLLPPL EYLMYLNTA	32 42 106 94 268 381 371 157 242 433 594 386 367 159 51 125 614 429 355	300 200 150 50 28 25 24 24 24 20 17.28 15.84 14.4 12 10.8 10.08 10 9.6 9.6
	YLPEFLTNC ILWDLDHLT ALQGGSFDV MQYPVFPWV ALYGHTQAV YLVRMPPFT VLMTFENLA ILAVERNKV ELTPEFFYL YLMYLNTAA VLADYTSET RMFHSVKST SNFEYLMYL KVLMTFENL LLPPLWNRT QLFTKPHPA GAHLSLWNV WDLDHLTHV FISLHRKAL CILWDLDHLTHV FISLHRKAL CILWDLDHL SEQUENCE VLLPPLWNR CLGSYGSDK CVWELSMTK GLRLRQALY NLANPKIFR RVWKTEDVK QVPKQLFTK RMPPFTQAF KLKFIQRFK TILGFVSNF SLPGHPQPF WIDLIFGYK NLHHWIDLI YMQYPVFPW ELTPEFFYL ALYGHTQAV YLPEFLTNC ITVASYLVR DMTVQCHYY QLFTKPHPA SEQUENCE QYPVFPWVL DYTSETLNL SYLVRMPFF YYTHYSSAI NFGQVPKQL SYGSDKVLM GFDDFSCCL EFFYLPEFL YFYGDRMQL RGLRLRQAL KNLALSREL KVLMTFENL TFSWGFDDF FYLPEFLTN ANPKIFRDL SFDVADRMF KTSPAVTAL KGRPGLRLL KKSPRGLRL KKSPRGLRL KKSPRGLRL RNKVLLPPL	YLPEFLINC

EDID ND. 10847

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-1.TXT Beginning with residue: 1 and ending with residue: 1270 AMPHI Window size: 11

- A AMPHI mid points of blocks.

 R Residues matching the Rothbard/Taylor motif.

 D Residues matching the IAd motif.

D d	- Residues mate	ching the I	Ad motif. Ed motif.	-			
						60 65	70 75
RD	5 10 15 OFQSEVLLSAMELFHI	20 25 MTSGGDAAMFR	TOUR PROPERTY	EAAAADST.A	50 55 NISCFTQKLV	EKLYSGMFSADI	RHILLFIL
			• • • • • • • •	AAAA.A	AAAAAA	AAAAAAAA	
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				100	125 120	135 140	145 150
737	80 85 90 HIMVVIETASSQRDT	W.T.P.P.V.TTP.TV	TANCE SEE	COSTSECIA	125 130 LLSILGFLOE	HWDVVFATYNSI	NISFLLCLM
		ααααααα	. 2	ΙΑΑΑΑΑΑΑΑ	AAAAAAAAA	AAAA	
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	155 160 165	170 175	180 185	190 19	200 205	210 215	
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	305 310 315 OPECKTEDFVSCIEN	320 325	330 335	340 34 KCCNTKAAN	5 350 350	SELGLWSOGEET	KPCSPWELD
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	380 385 390	395 400	405 410	415 42	0 425 43	0 435 440	445 450
W	380 385 390 WREGPARMRKRIKRL AAAAAAAAAAA	SPLEALSSGRH	KESQDKNDH	ISQTNAEN	DELTLREAEG	RPDEAGADG1Ø1	AAAA AAAA.
		aaaa			RRRRR		
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1	t tropper et opppost	TIARLINKEK	MOKESTATI	<i>I</i> OCHLVSEG	<i>T</i> LLFGHOHFYI	CENTTLSPIGD	VYCTRHCLSN
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	TARRETTEM CCVDDC	ייייטנועפרערשפי	VADMPET.PO	A T CIOLTATE A	LETFFHNGYSK	FLVFYNNDRSK	AFKSFCSFQP
		ממ	ασασασσα				.AAAAAA
	A.AAAAA			.RRRRRRR	RRRRRR		RRR
	605 610 615 SLKGKATSEDTLNLI	620 625	630 63	5 640 6	45 650 65 TAACDTCNTV	55 660 665 MOYDVFDWVT.&T	670 675 YTSETINLAN
	7.7	***	272		. AAAAAAAAA	A. <i></i>	
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	DETERMINE CENTRAL	ጥሆ₽₽ ₽₹.₽₽₹^₽	PKEVEKTEG	DMTVOCHYS	THYSSAIIVA	SYLVRMPPFTQ/	FLCATORGEL T
	AAAAAAAAAAAAA	AAAAA	AAAAAA	RRRRR RPR	RR		F
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755	760	765	770	775	780	785	790	795	800	805	810	815	820	825
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005	910	915	920	925	930	935	940	945	950	955	960	965	970	975
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ANALYSIS	RESULTS	OF	THE	PROGRAM	TSITES.
******	******	***	****	******	*****

These are the results of the analysis of the file --> LY1484~2.TXT Beginning with residue: 1 and ending with residue: 647 AMPHI Window size: 11

- A AMPHI mid points of blocks.

 R Residues matching the Rothbard/Taylor motif.

 D Residues matching the IAd motif.

 d Residues matching the IEd motif.

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	20 · 25	20 21	- 40	45 50	n 55	60 61	70	75
5 10 15 MLQKWQKRDISNFEYI	20 '25	: 5 U S	ว 4.U เทรานสาราชา	TALTTUDOTO	LANDKI FR	DT.SKPMG/	OTKERKLE	
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RRRRR		DDDDD	• • • • • • •	• • • • • • •	• • • • • • •	• • • • • •	• • • • • • • •	• • •
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155 160 165		100 10	- 100	105 20	0 205	210 21	5 220	225
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230 235 240	245 250	255 26	0 265	270 27	5 280	285 29	0 295	300
TOO CONTRACTOR VINITED	IDVEVGDEMDT.S	CTTOOT.TR	COTTLORY	SNEGOVPK	COLFTKPHI	PARTAAGK	TPLCKDA2	TPV
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				245 25	-0 355	260 36	5 370	375
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455 460 46	- 450 456	400 4	05 400	40E E	00 505	510 5	15 520	525
455 460 46 LAASVTFSLLVSGS	5 470 475	480 4	DE 430	C CCP VODITIES	SCTTVSCA	GAHLSLW	NVNGOPLA	SITT
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605 610 61	E 630 601	. 620	635 <i>64</i> 0	645	550 655	660 6	65 670	675
605 610 61 ELDVSIALTGKPS	.D 620 625 PRODATEST	י ספט פ מודאיים	ಗಡಬಿಡವಿದಿಬ ಗಡಬಡವಿದಿಬ	FCWSADG				
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Ly1456P LifeSeqGold Clone Distribution

Ly1456P LifeSeq Gold Search

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** = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred. * = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).

ORF#1 = 379>672 = 294bp = 98aa ORF#2 = 555>734 = 177bp = 59aa ORF#3 = 1037>1291 = 252bp = 84aa ORF#4 = 1074>1274 = 198bp = 66aa

SEQ ID NO: 10,475

1 gtcttctccc	tgtgtcttca	cataatcccc	gctgtctgtg	cgttgtgccc	tgatctcctc
61 ttcttataag	gaccccaatc	atattggatt	agagcccatc	cacaggacct	aaatttttcc
121 cttaactctt	ffcctattta	ccccaagaac	actcaccage	agetettgeg	gctgcagcgt
181 ttaccccaaa	ataatttaat	cacaaaacat	ctccctttta	ttattttcac	tttgctttag
161 CLaccccaaa	gtaatttggt	cacaaaacac	tatacatata	agacatcatt	ctaddtatad
241 tgtatcaact	ttggaaacaa	aayacaccac	teracgeaca	agacaccacc	ccaggeacag
301 cgttctgtct	ttagtagtgg	catttccatt	tagaaaatat	agtaattete	gattyctyda
361 aatgtcaaat	ccgagaaaac	atagcattcc	tatgtgatca	ttctcaaaga	grigitggee
421 aaagattcat	ttgattaatc	ctatttttct	gaaatagacg	attctgatga	ttgagatgat
481 tttgatgtta	attctattta	cacataactc	caaqaacagt	ttttaaattt	tactttcaca
541 ttgaaaatca	atcagattag	tttatqtaaa	attaaatgag	ctctqqccaa	qcacqqtqqc
601 tcatgcctat	aataccacca	ctttaggaag	ctgaggtgga	cagatcactt	gaggtcagga
661 gtttgacacc	aaccccagca	acetagggagg	acccatata	tacaaaaaat	acatatatat
661 gtttgatace	agucugggca	gcacggcgaa	accecgeeee	anganagata	2000000000
721 tagccagatg	tggtggtgca	tgeetgtggt	eccagettet	caggaageeg	aggcaggaga
781 atcatttgaa	cttgaggggc	agaggttgca	gtgagccaag	attgtgccat	ggaaccccaa
841 cctgggcaac	agagcaagac	tctgtctcaa	aaaaaaaaa	aaatgctggc	agtgggctgc
901 acttttttt	ttcctaaaca	ggaaaagggt	taattatttc	tttaaagaac	ctagcaccaa
961 atacagtcac	attcggaggt	actgggggtt	gggacttgaa	catatgaatt	ttggagggc
1021 acaaggcatc	ccatgacaca	totoggaacc	ggtataatct	ctacagagac	tagaatttag
1081 atttaacagc	ttgaaacagg	ttcaagttat	tootaacata	caaaacaaaa	acaattcaaa
1141 gccctttaca	ttgaaattat	traataaaaa	ataactattt	ctacaatota	taaaaggtat
1141 gecetttata	tttaaattat	tyaacaaaaa	tataatttta	tatttaatta	cadaaaaattc
1201 gctatgttta	ttagtettae	Ligiagolaa	CCCacccca	cycliccia	tagaaaaccc
1261 ttgacatttt	atgtttccgt	gtaagagatt	gtacagaagg	caaacccccg	Lyctatycaa
1321 taataatact	ctaatacaaa	ttctgttatg	aacttcattg	gcactatatt	taaatgtcat
1381 agcaattatt	tttatgtggt	attttcaaat	aatctagatt	tcatgcagca	ttataaaact
1441 aactggggct	ggggacactg	gctcatgcct	qtaatctcaa	cactttggga	ggccaaggcg
1501 ggcagactgc	ttaagcccag	gagtttgaga	ccatcctqqq	caacatggca	aaaccccgtc
1561 totacaaaaa	atacaaaaca	aaacaaaatt	agccagacat	gatagtacac	acctataatc
1621 ccagctacto	acacaaaaca	Cacacacaca	tcacttcaac	accoccacca	gaggttggag
1621 Ccagctactc	aggaggetga	cacaggagga	tractigaac	acgggaggca	tatatassas
1681 tgagccagga	ttgtgccact	gcattccagc	Egggtgacac	agegagaeee	cyccicaaaa
1741 caaaacaaa	caaaacaaaa	acaaaacaga	aaacagtgtg	agaagtgttc	attacccacc
1801 cacccccacc	cccaaagctt	tccaagctcc	cgaccccata	cagaggcaaa	ggatgcactg
1861 tocaaaocto	cctacctaac	cccaaacqtc	cagtcaaacc	caccactgcc	cttgcatgac
1921 ttctgacccc	tccaccttca	atctagaccc	cacacctatc	ccaccatcat	ctcaagccaa
1981 gggggacctt	gaataaaggt	tttcttcctq	tecetacace	tccagacaag	agagtgcaat
2041 ggtttcttag	gaacaaagge	tectettaaa	acatttaaca	aggtcaagat	aacttaaaat
2101 agttaccaga	acagaccaga	tagagtagta	gatggagagg	aggreactes	gacatgggat
2101 agttaccaga	Caaaaacaya	tygactagta	catggatagt	tagecaacega	atacacagaa
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SER JONO: 10,476

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SER JD NO: 10,477

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Ly1488 Protein Sequence (SERID NO: 10,969)

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TMpred Report for Ly1488 (SERIAND: 10,969)

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Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains Transmembrane Domain 1: 199 - 220 Score: 1.3061

Ly1449 and Ly1480 matches Lung cancer associated polynucleotide sequence SEQ ID 10,476

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Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)

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			agccaagtgg			
			ctcctcactg			
			aacgttaaat			
			tgtatcacaa			
			aagggagctg			
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			tttcagtggc			
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Detection of Ly 1448P specific serum antibodies in lymphoma patients

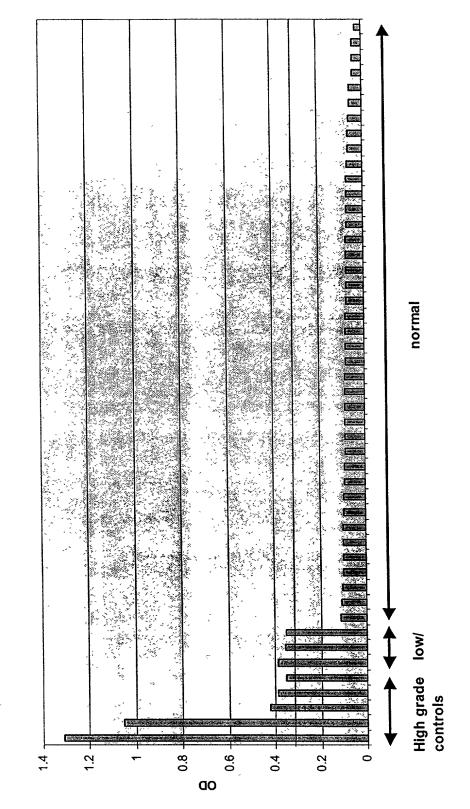


Figure 31

Detection of TCL-1 specific serum antibodies in lymphoma patients

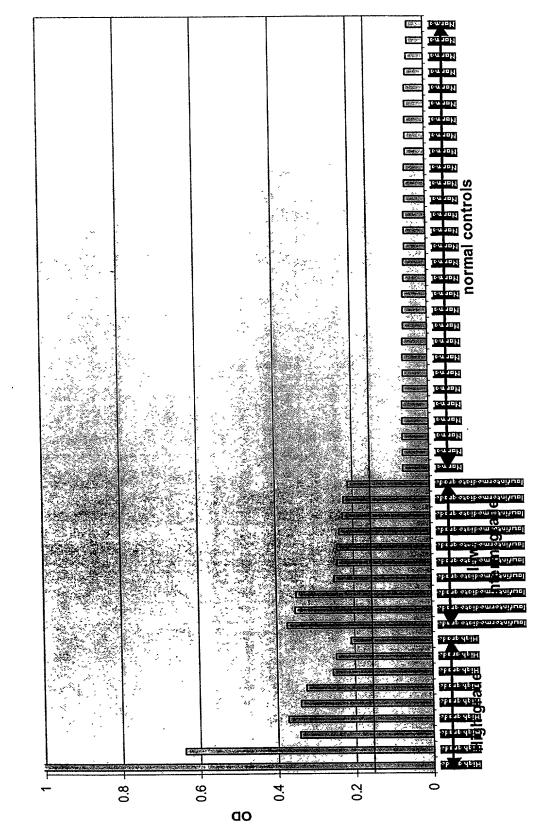


figure 3